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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/720,096	02/01/2001	Dan Nilsson	54337.000009	6906

21967 7590 05/16/2006

HUNTON & WILLIAMS LLP
INTELLECTUAL PROPERTY DEPARTMENT
1900 K STREET, N.W.
SUITE 1200
WASHINGTON, DC 20006-1109

EXAMINER

STEADMAN, DAVID J

ART UNIT PAPER NUMBER

1656

DATE MAILED: 05/16/2006

Please find below and/or attached an Office communication concerning this application or proceeding.



UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, DC 20231
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APPLICATION NO. / CONTROL NO. 09/720,096	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER David J. Steadman

ART UNIT	PAPER
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1656

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents

The communication filed **2/28/2006** is not fully responsive to the Office communication mailed 12/29/2005 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.


Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner **David J. Steadman**, Art Unit **1656**, whose telephone number is **(571) 272-0942**.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Kathleen Kerr, can be reached at **(571) 272-0931**.

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is **(571) 272-1600**.

David J. Steadman


DAVID J. STEADMAN, PH.D.
PRIMARY EXAMINER

Notice to Comply	Application No.	Applicant(s)	
	Examiner	Art Unit 1656	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", **as well as an amendment specifically directing its entry into the application.**
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216 or (703) 308-2923

For CRF Submission Help, call (703) 308-4212 or 308-2923

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/720,096A
Source: IFW/b
Date Processed by STIC: 3/3/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

*Per 1.824 of Sequence Rules
submit only one file in
computer readable form.*



IFW16

RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/09/720,096A

TIME: 10:34:36

Input Set : E:\Sequence Listing\9810089_final.txt

Output Set: N:\CRF4\03032006\I720096A.raw

2 <110> APPLICANT: Dan Nilsson
3 Thomas Janzen
W--> 4 <120> TITLE OF INVENTION: Method of preventing bacteriophage
W--> 5 infection of bacterial cultures
7 <130> FILE REFERENCE: 21134 PC 1
C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/720,096A
C--> 8 <141> CURRENT FILING DATE: 2001-01-02
8 <150> PRIOR APPLICATION NUMBER: PA 1998 00878
9 <151> PRIOR FILING DATE: 1998-07-03
10 <150> PRIOR APPLICATION NUMBER: US 60/091,735
11 <151> PRIOR FILING DATE: 1998-07-06
E--> 12 <160> NUMBER OF SEQ ID: 6 *(see p.4)*
13 <170> SOFTWARE: FastSEQ for Windows Version 3.0

*Suggestion!
Consult
sequence
rules
for valid
format.*

ERRORED SEQUENCES

15 <210> SEQ ID NO: 1
16 <211> LENGTH: 32
17 <212> TYPE: DNA
18 <213> ORGANISM: Artificial Sequence
W--> 19 <220> FEATURE:
20 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
21 deletion in thyA from strain CHCC373
W--> 22 <400> SEQUENCE: 1
E--> 23 tataatctgc agggtcacac tatcagtaat tg

**Does Not Comply
Corrected Diskette Needed**

*32 ← insert cumulative
base total at
right margin of each
line*

09/720,096A 2

<211> 4815

<212> DNA

<213> Lactococcus lactis subsp. cremoris

<213> STRAIN: MG1363

<400> 7

TATCTCGCTA AGTTAGGAGA ATAAG ATG ACA AAA GTA AAT TCA CAA AAA TAG
Met Thr Lys Val Asn Ser Gln Lys Tyr

do NOT show 2 <2137> line,
per sequence rules.

→ <2207> insert

<2237> put
52 response
on this
line.

show lower-case letters
for nucleotides

show any explanatory
information in the
<2207-2237
section.

insert <2207> first.
It is a "header"
and never has a
response. Then,
insert <2237> and
put "STRAIN: MG1363"
on that line

use lower-case letters
for nucleotides

09/720, 096A 3

↓
<210> 8
<211> 2207
<212> DNA
<213> Lactococcus lactis subsp. lactis
<400> 8

TGA TTC TAC TTA CAT TCA CGT CTT TTG GAA CGT GCT GCC AAA TTA TCT
Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser
470 5 475 10 480 15

48

Per 1.822 of sequence rules, number
the amino acids (in a mature protein)
beginning with "1", even if they're in a coding
sequence.

Please follow above example in re-numbering
amino acids. Same error in sequences 9,
10, and 11.

09/720,096A

4

<210> 11 last sequence is submitted file
<211> 375
<212> DNA
<213> Trichoderma reesei
<400> 11

TACTCGAAGA ATTCGGCAG AGGCTGATTG CTCTCGGTCA TCTGCCAAG ATG TTC

Met Phe
260

55

use lower-case letters

and →
re-do numbering

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/720,096A

DATE: 03/03/2006

TIME: 10:34:37

Input Set : E:\Sequence Listing\9810089_final.txt

Output Set: N:\CRF4\03032006\I720096A.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
 L:8 M:270 C: Current Application Number differs, Replaced Current Application No
 L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:12 M:283 W: Missing Blank Line separator, <160> field identifier
 L:19 M:283 W: Missing Blank Line separator, <220> field identifier
 L:22 M:283 W: Missing Blank Line separator, <400> field identifier
 L:23 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:1
 L:29 M:283 W: Missing Blank Line separator, <220> field identifier
 L:32 M:283 W: Missing Blank Line separator, <400> field identifier
 L:39 M:283 W: Missing Blank Line separator, <220> field identifier
 L:42 M:283 W: Missing Blank Line separator, <400> field identifier
 L:49 M:283 W: Missing Blank Line separator, <220> field identifier
 L:52 M:283 W: Missing Blank Line separator, <400> field identifier
 L:59 M:283 W: Missing Blank Line separator, <220> field identifier
 L:63 M:283 W: Missing Blank Line separator, <400> field identifier
 L:70 M:283 W: Missing Blank Line separator, <220> field identifier
 L:74 M:283 W: Missing Blank Line separator, <400> field identifier
 L:82 M:280 W: Numeric Identifier already exists, Organism not replaced.
 L:83 M:283 W: Missing Blank Line separator, <400> field identifier
 L:84 M:112 C: (48) String data converted to lower case,
 M:112 Repeated in SeqNo=7
 L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:232 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:375 M:283 W: Missing Blank Line separator, <400> field identifier
 L:376 M:112 C: (48) String data converted to lower case,
 L:378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
 M:112 Repeated in SeqNo=8
 L:381 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
 L:384 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8

6

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/720,096A

DATE: 03/03/2006

TIME: 10:34:37

Input Set : E:\Sequence Listing\9810089_final.txt

Output Set: N:\CRF4\03032006\I720096A.raw

L:387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:390 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:393 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:396 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:402 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:405 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:408 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:414 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:475 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:517 M:283 W: Missing Blank Line separator, <400> field identifier
L:518 M:112 C: (48) String data converted to lower case,
L:520 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
M:112 Repeated in SeqNo=9
L:523 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:529 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:535 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:541 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:547 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:550 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:553 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:559 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:656 M:283 W: Missing Blank Line separator, <400> field identifier
L:657 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=10
L:714 M:283 W: Missing Blank Line separator, <400> field identifier
L:715 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=11
L:12 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (6) Counted (11)